

Please amend the application as follows:

In the Specification

Please replace the paragraph at page 9, lines 7 through 17 with the following paragraph:

Fig. 3 shows a table providing detailed information about the SNPs identified herein. Column one shows the internal polymorphism identifier. Column two shows the accession number for the reference sequence in the TIGR database which can be found on the world wide web at tigr.org/tdb/hgi/searching/hgi_reports.html. Column three shows the nucleotide position for the SNP site. Column four shows the gene in which the polymorphism was identified. Column five shows the polymorphic site and additional flanking sequence on each side of the polymorphism. Column six shows the type of mutation produced by the polymorphism. Columns seven and eight show the reference and alternate (variant) nucleotides, respectively, for the SNP. Columns nine and ten show the reference and alternate (variant) amino acids, respectively, encoded by the alleles of the gene.

Please replace the paragraph at page 14, line 25 to page 15, line 21 with the following paragraph:

The invention also relates to nucleic acid molecules which share substantial sequence identity to the variant alleles identified herein (or their complements) and which also comprise the variant nucleotide at the SNP site. Particularly preferred are nucleic acid molecules and fragments which have at least about 60%, preferably at least about 70, 80 or 85%, more preferably at least about 90%, even more preferably at least about 95%, and most preferably at least about 98% identity with nucleic acid molecules described herein. The percent identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (e.g., gaps can be

introduced in the sequence of a first sequence). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 60%, and even more preferably at least 70%, 80% or 90% of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.*, 25:389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used. See the world wide web at ncbi.nlm.nih.gov. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

Please replace the paragraph at Page 48, lines 1 through 12 with the following paragraph:

Publicly available sequences for a given gene were assembled into Gap4, which can be found on the world wide web at biozentrum.unibas.ch/~biocomp/staden/Overview.html. PCR primers covering each exon were designed using Primer 3, which can be found on the world wide web at genome.wi.mit.edu/cgi-bin/primer/primer3.cgi. Primers were not designed in regions where there were sequence discrepancies between reads. Genomic DNA was amplified in at least 50 individuals using 2.5 pmol each primer, 1.5 mM MgCl₂, 100 μM dNTPs, 0.75 μM AmpliTaq GOLD polymerase, and 19 ng DNA in a 15 μl reaction. Reactions were assembled using a PACKARD MultiPROBE robotic pipetting station and then put in MJ 96-well tetrad thermocyclers (96°C for 10 minutes, followed by 35 cycles of 96°C for 30 seconds, 59°C for 2 minutes, and 72°C for 2 minutes). A subset of the PCR assays